

Supplemental material

(a)

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.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130
1  MIVTVSSR--RPSPPVQNL LLHPLSKSSL QTFHFP--FS LMRLIV--C PASVVRGLLF LEDTPGHLSL LSGKPNPDTF PFTSFTEFAR SPINSKEDAL ITTECKELAQ GLQYGFAGE KQLLSWIEGL
2  NSQIFDTS-----ISHDAP VRRLKRYNT DFLSDIAKRF KPSAIRSLFH LHPHGLISL LAGKPNPDTF PFTSISEFAR SEVHBEETIT INLSGADLAQ GLQYGDYAGI KQLLDWIYGL
3  MIOISDTN-----SHDAP VRRLKRYNT NFLSNIAKRF KPSAIRSLFH LHPHGLISL LAGKPNPDTF PFTSISEFAR SEGHSDBEIT INLSGADLAQ GLQYGDYAGI KQLLDWIYGL
4  MKKSTDSGE INGS-----OPLTSSDG VKVLEDAFYT SFLSDIAKRF KPSAIRSLFH LHPHGLISL LAGKPNPDTF PFTSISEFAR DPLNPDRTDA ITTDCPALAQ GLQYGDYAGI HGLLDWIYGL
5  MPKEANG-----NGISD VKVLEDAFYT PFLSEANRF KPSAIRSLFH LHPHGLISL LAGKPNPDTF PFTSISEFAR SEVHBEETIT LEVDKADLR GLQYGMAGD SSIIVNWIEGL

.....140.....150.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260
1  QEPFHGRKRN EGWRVSIIGCG SQDLIKAVT AVVNPQDSVL LEPHYVAF FVVPHPILLN MGCVWVGLI YIFAA-----I YRKLASROAK ACGFVYSECK DVDIRQRYCC NPTGTMATLE RRKEVILLAR
2  QBINHGRKRN EGWRVSIIGCG SQDLIKAVT AVVNPQDSVL LEPHYVAF FVVPHPILLN MGCVWVGLI YIFAA-----I YRKLASROAK ACGFVYSECK DVDIRQRYCC NPTGTMATLE RRKEVILLAR
3  QBINHGRKRN EGWRVSIIGCG SQDLIKAVT AVVNPQDSVL LEPHYVAF FVVPHPILLN MGCVWVGLI YIFAA-----I YRKLASROAK ACGFVYSECK DVDIRQRYCC NPTGTMATLE RRKEVILLAR
4  QEAQHGRKRG EGWRVSVGAG SQDLIKAVA AVVNPQDSVL LEPHYVAF FVVPHPILLN MGCVWVGLI YIFAA-----I YRKLASROAK ACGFVYSECK DVDIRQRYCC NPTGTMATLE RRKEVILLAR
5  QEPFHGRKRG EGWRVSVGCG SQDLIKAVT AVVNPQDSVL LEPHYVAF FVVPHPILLN MGCVWVGLI YIFAA-----I YRKLASROAK ACGFVYSECK DVDIRQRYCC NPTGTMATLE RRKEVILLAR

.....270.....280.....290.....300.....310.....320.....330.....340.....350.....360.....370.....380.....390
1  EHNFIILEGM DPYFYLKYG TAPRPSYFA LELEPEVGR VLRFDLSKV LSAGIRIGVF SGPEPILVAI DQHTSINLQ TFSLTQIHH KLLNSWGYC BATHVNVAV FYREKRDIFF RAMRHHISGL
2  EHNFIILEGM DPYFYLKYG TAPRPSYFA LELEPEVGR VLRFDLSKV LSAGIRIGVF SGPEPILVAI DQHTSINLQ TFSLTQIHH KLLNSWGYC BATHVNVAV FYREKRDIFF RAMRHHISGL
3  EHNFIILEGM DPYFYLKYG TAPRPSYFA LELEPEVGR VLRFDLSKV LSAGIRIGVF SGPEPILVAI DQHTSINLQ TFSLTQIHH KLLNSWGYC BATHVNVAV FYREKRDIFF RAMRHHISGL
4  EHNFIILEGM DPYFYLKYG TAPRPSYFA LELEPEVGR VLRFDLSKV LSAGIRIGVF SGPEPILVAI DQHTSINLQ TFSLTQIHH KLLNSWGYC BATHVNVAV FYREKRDIFF RAMRHHISGL
5  EHNFIILEGM DPYFYLKYG TAPRPSYFA LELEPEVGR VLRFDLSKV LSAGIRIGVF SGPEPILVAI DQHTSINLQ TFSLTQIHH KLLNSWGYC BATHVNVAV FYREKRDIFF RAMRHHISGL

.....400.....410.....420.....430.....440.....450.....460.....470.....480.....
1  AEWSPFAAG FFWFKLLLD EPGEDE--D SYVILSRGI ERGVIALPQA GFEPNSRRTA YVRSFSAAP BEVDEAIRR LRDAILDARA TNKK---
2  AEWSPFAAG FFWFKLLLD NKAADDDSD SEVWIKTKAF ERGVIALPQT VFLPNCRTP YVRASFSLTG EDVDRAIOR IRDAILDARA TAVAIPI
3  AEWSPFAAG FFWFKLLLD NKAADDDSD SEVWIKTKAF ERGVIALPQT VFLPNCRTP YVRASFSLTG EDVDRAIOR IRDAILDARA SVNGISA
4  AEWSPFAAG FFWFKLLLD QDGA---GD SSVIIRTKAL ERGVIALPQT VFLPNCRTP YVRASFSLTG BEVWEAIRR LRDAILDARA AKLS-TV
5  AEWSPFAAG FFWFKLLLD TGASDE--D SEVWIKTKAF ERGVIALPQT VEPNNSRRTA YVRASFSLTG EQOIDEAIRR LRDAILDARA ASTAGKA
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(b)

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.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130
1  M--SSS--EAT LQAEVDRLRN EYVQVKEEQL GRSTKLSIGN YLLRRLAQLG IIVRQSMFGV PGDFNLGFLV RVFFVYQDLV BEHEFDWVG NWCYCLGLSLY LLYAADRTDR CNELNAYAA DGYARVKE-S
2  MATTS--AES LQAEVNRIRI EYVQVKEEQL GSECIYIGD YLLRRLAQLG VT---SMFGV PGDFNLGFLV -----DLV EDHFDWVG N----- CNELNAYAA DGYARVKEGS
3  MASOT--VAA LQAEVDRIRI EYVQVKEEQL GSECIYIGD YLLRRLAQLG AN---SMFGV PGDFNLGFLV -----DLV EDHFDWVG N----- CNELNAYAA DGYARVKEGS
4  M--SNE--EAT LQAEVDRIRI EYVQVKEEQL GSECIYIGD YLLRRLAQLG VT---SMFGV PGDFNLGFLV -----DLV EDHFDWVG N----- CNELNAYAA DGYARVKEGS
5  M--SSHPASV LQAEVDRIRI EYVQVKEEQL GSECIYIGD YLLRRLAQLG VT---SMFGV PGDFNLGFLV -----DLV EDHFDWVG N----- CNELNAYAA DGYARVKEGS

.....140.....150.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260
1  IGVVLTTFGV GELSAINGIA GAFSEMFPVL HIVGVVSTAC QKAKFLHHT LGDGRVYVIR HVT--EHRHD SLIDTHTMTR LQNNRIR-- COARFVVL VFNVLVAKI SSAPRTPIN RPPPNRDE
2  IGVVLTTFGV GELSAINGIA GAFSEMFPVL HIVGVVSTAC QKAKFLHHT LGDGRVYVIR HVT--EHRHD SLIDTHTMTR LQNNRIR-- COARFVVL VFNVLVAKI SSAPRTPIN RPPPNRDE
3  IGVVLTTFGV GELSAINGIA GAFSEMFPVL HIVGVVSTAC QKAKFLHHT LGDGRVYVIR HVT--EHRHD SLIDTHTMTR LQNNRIR-- COARFVVL VFNVLVAKI SSAPRTPIN RPPPNRDE
4  IGVVLTTFGV GELSAINGIA GAFSEMFPVL HIVGVVSTAC QKAKFLHHT LGDGRVYVIR HVT--EHRHD SLIDTHTMTR LQNNRIR-- COARFVVL VFNVLVAKI SSAPRTPIN RPPPNRDE
5  IGVVLTTFGV GELSAINGIA GAFSEMFPVL HIVGVVSTAC QKAKFLHHT LGDGRVYVIR HVT--EHRHD SLIDTHTMTR LQNNRIR-- COARFVVL VFNVLVAKI SSAPRTPIN RPPPNRDE

.....270.....280.....290.....300.....310.....320.....330.....340.....350.....360.....370.....380.....390
1  BAVVLDLHNR QVREAGDGVV VIVDACVIRH CVREAVDQL RKTGFVYAA PMGRTAVDEE YERYGGIYVC SLTPEIRK VESAKLISHI GSKLSDFNTC NFSYKPTUR TIE----- YAVAGVG
2  BAVVLDLHNR QVREAGDGVV VIVDACVIRH CVREAVDQL RKTGFVYAA PMGRTAVDEE YERYGGIYVC SLTPEIRK VESAKLISHI GSKLSDFNTC NFSYKPTUR TIE----- YAVAGVG
3  BAVVLDLHNR QVREAGDGVV VIVDACVIRH CVREAVDQL RKTGFVYAA PMGRTAVDEE YERYGGIYVC SLTPEIRK VESAKLISHI GSKLSDFNTC NFSYKPTUR TIE----- YAVAGVG
4  BAVVLDLHNR QVREAGDGVV VIVDACVIRH CVREAVDQL RKTGFVYAA PMGRTAVDEE YERYGGIYVC SLTPEIRK VESAKLISHI GSKLSDFNTC NFSYKPTUR TIE----- YAVAGVG
5  BAVVLDLHNR QVREAGDGVV VIVDACVIRH CVREAVDQL RKTGFVYAA PMGRTAVDEE YERYGGIYVC SLTPEIRK VESAKLISHI GSKLSDFNTC NFSYKPTUR TIE----- YAVAGVG

.....400.....410.....420.....430.....440.....450.....460.....470.....480.....490.....500.....510.....520
1  MKQLLEKITE KLVSYRDRAS HIEVREFFNT VNEGDDKHT HSEWFRVGD FFKPKDVIIT ERGTSFGIL EVPLPESVL VQQLWGSIG WVGSTLGA LAARDVGLGR TILFVGDGSL QLVQVQLSM
2  MKQLLEKITE RLHPFNAEAR KIEVREBAVH LEDNDKREIT HAWLWFRMAN FFKPKDVIVA ETGTSFGIL DVPLPESVL VQQLWGSIG WVGSTLGA LAARDVGLGR TILFVGDGSL QLVQVQLSM
3  MKQLLEKITE RLHPFNAEAR KIEVREBAVH LEDNDKREIT HAWLWFRMAN FFKPKDVIVA ETGTSFGIL DVPLPESVL VQQLWGSIG WVGSTLGA LAARDVGLGR TILFVGDGSL QLVQVQLSM
4  MKQLLEKITE RLHPFNAEAR KIEVREBAVH LEDNDKREIT HAWLWFRMAN FFKPKDVIVA ETGTSFGIL DVPLPESVL VQQLWGSIG WVGSTLGA LAARDVGLGR TILFVGDGSL QLVQVQLSM
5  MKQLLEKITE RLHPFNAEAR KIEVREBAVH LEDNDKREIT HAWLWFRMAN FFKPKDVIVA ETGTSFGIL DVPLPESVL VQQLWGSIG WVGSTLGA LAARDVGLGR TILFVGDGSL QLVQVQLSM

.....530.....540.....550.....560.....570.....580.....590.....600.....610.....620.....630
1  IRKGLKPIIE VLNNSGYTIE RLTHGRNRY NDLSNWKVIA LRSVFGDPE RUSAFVTNT KGLSKLLDD AIFARAKTIC LVEVMMKFD APRALQVQA LSA-----
2  IRKGLKPIIE VLNNSGYTIE RLTHGRNRY NDLSNWKVIA LRSVFGDPE RUSAFVTNT KGLSKLLDD AIFARAKTIC LVEVMMKFD APRALQVQA LSA-----
3  IRKGLKPIIE VLNNSGYTIE RLTHGRNRY NDLSNWKVIA LRSVFGDPE RUSAFVTNT KGLSKLLDD AIFARAKTIC LVEVMMKFD APRALQVQA LSA-----
4  IRKGLKPIIE VLNNSGYTIE RLTHGRNRY NDLSNWKVIA LRSVFGDPE RUSAFVTNT KGLSKLLDD AIFARAKTIC LVEVMMKFD APRALQVQA LSA-----
5  IRKGLKPIIE VLNNSGYTIE RLTHGRNRY NDLSNWKVIA LRSVFGDPE RUSAFVTNT KGLSKLLDD AIFARAKTIC LVEVMMKFD APRALQVQA LSA-----
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(c)

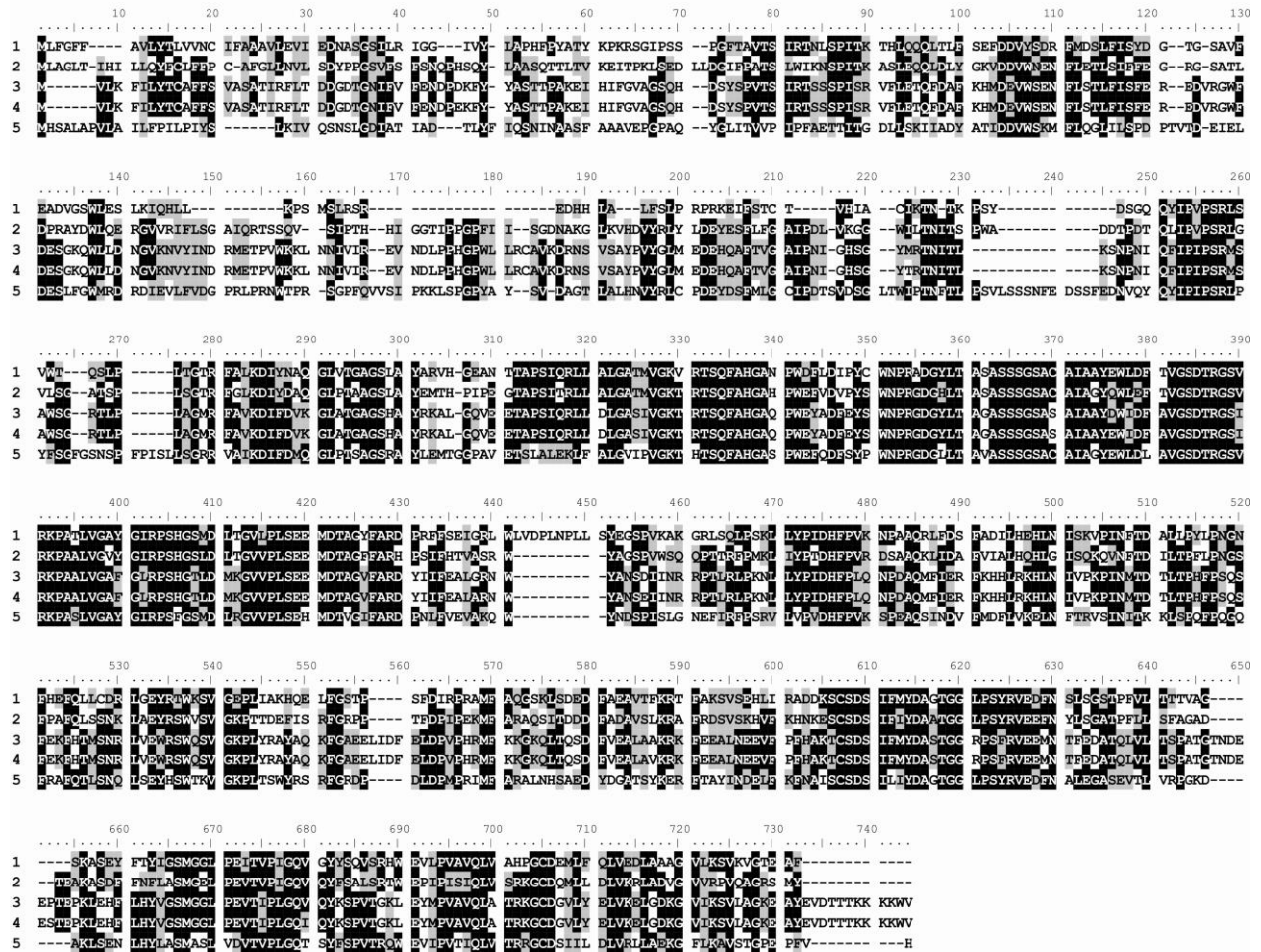


Fig. S1: Alignments for identification of IAA biosynthesis genes from *T. vaccinum*. Conceptually translated sequences for *tam1*, *ipd1* and *iah1* were aligned with four most similar sequences in BLASTp using MAFFT and BioEdit alignments. *Tam1* (1: KP096350) was aligned to sequences 2 (KDR75974 of *Galerina marginata*), 3 (KDQ24236 of *Pleurotus ostreatus*), 4 (KDR77824 of *Galerina marginata*) and 5 (XP_007868862 of *Gloeophyllum trabeum*) (a), *Ipd1* (1: KP096351) was aligned to 2 (XP_007845706 of *Moniliophthora roreri*), 3 (KDQ25837 of *Pleurotus ostreatus*), 4 (KDR82740 of *Galerina marginata*) and 5 (XP_001875889 of *Laccaria bicolor*) (b); *Iah1* (1: KP096352) was similar to 2 (KDR84180 of *Galerina marginata*), 3 (XP_007329104 of *Agaricus bisporus*), 4 (XP_006456935 of *Agaricus bisporus*) and 5 (XP_007846638 of *Moniliophthora roreri*) (c).

Tab. S1: Orthologs in mycorrhizal, plant-pathogenic/parasitic as well as saprobic fungi for the enzymes Tam1, Ipd1, Ald1 and Iah1 suggested to be involved in IAA production in *T. vaccinum* (protein-IDs, JGI <http://genome.jgi-psf.org>, in brackets).

Protein	Mycorrhizal	Plant-pathogenic/parasitic	Saprobic
Tam1	<i>Laccaria bicolor</i> (191053); <i>Paxillus involutus</i> ATCC 200175 (103787); <i>Tricholoma matsutake</i> 945 (1422813); <i>Suillus luteus</i> UH-Slu-Lm8-n1 (801906)	<i>Armillaria mellea</i> (7757)	<i>Heterobasidion annosum</i> (458781); <i>Schizophyllum commune</i> H4-8 (2616666);
Ipd1	<i>Laccaria bicolor</i> (188370); <i>Paxillus involutus</i> ATCC 200175 (175618); <i>Tricholoma matsutake</i> 945 (1425307); <i>Suillus luteus</i> UH-Slu-Lm8-n1 (94806)	<i>Armillaria mellea</i> (6628)	<i>Heterobasidion annosum</i> (440059); <i>Schizophyllum commune</i> H4-8 (2626643); <i>Schizophyllum commune</i> H4-8 (2637783)
Ald1	<i>Laccaria bicolor</i> (256254); <i>Laccaria bicolor</i> (191009); <i>Paxillus involutus</i> ATCC 200175 (182543); <i>Paxillus involutus</i> ATCC 200175 (76843); <i>Tricholoma matsutake</i> 945 (1284147); <i>Tricholoma matsutake</i> 945 (1444458); <i>Tricholoma matsutake</i> 945 (1295949); <i>Tricholoma matsutake</i> 945 (1308658); <i>Suillus luteus</i> UH-Slu-Lm8-n1 (803802); <i>Suillus luteus</i> UH-Slu-Lm8-n1 (807535); <i>Suillus luteus</i> UH-Slu-Lm8-n1 (807087)	<i>Armillaria mellea</i> (9343); <i>Armillaria mellea</i> (5490); <i>Armillaria mellea</i> (3731); <i>Armillaria mellea</i> (13567)	<i>Heterobasidion annosum</i> (454399); <i>Schizophyllum commune</i> H4-8 (1156481); <i>Schizophyllum commune</i> H4-8 (2606953)
Iah1	<i>Tricholoma matsutake</i> 945 (290237)		

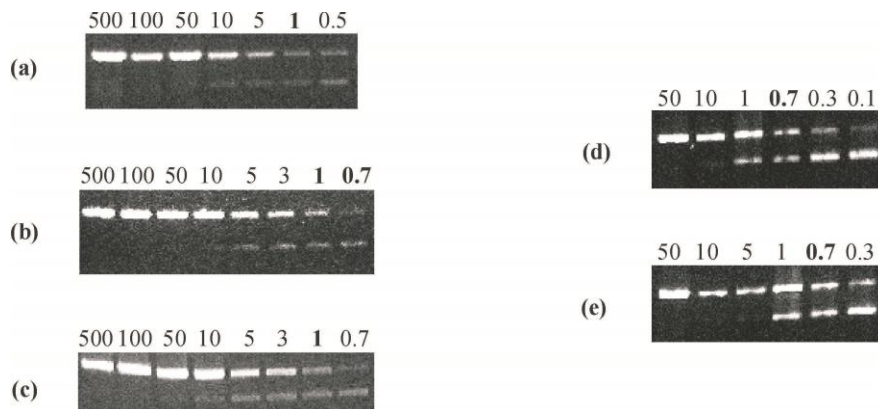


Fig. S2: Expression of *ald1* in *T. vaccinum* mycorrhiza. Competitive PCR was used to estimate the relative amount of the transcript using 1 ng cDNA for the control with mycelium from pure culture (a), and 0.02 ng fungal cDNA from mycorrhizal tissues Hartig' net (b) and hyphal mantle (c) from 3 weeks and (d) 3 months co-cultures with the compatible host, spruce and (e) the low compatible host, pine; the bold numbers indicate bands of the same intensity with the competitor. 1 pg *ald1* transcript was found in the pure culture, making it 10^{-3} of cDNA. In Hartig' net 0.7 to 1 pg was found making it 1:20 of all cDNA and thus approximately 40-fold more compared to pure culture. For mantle, 50-fold and in compatible interaction (45-fold) or for low compatibility (30-fold) can be calculated.

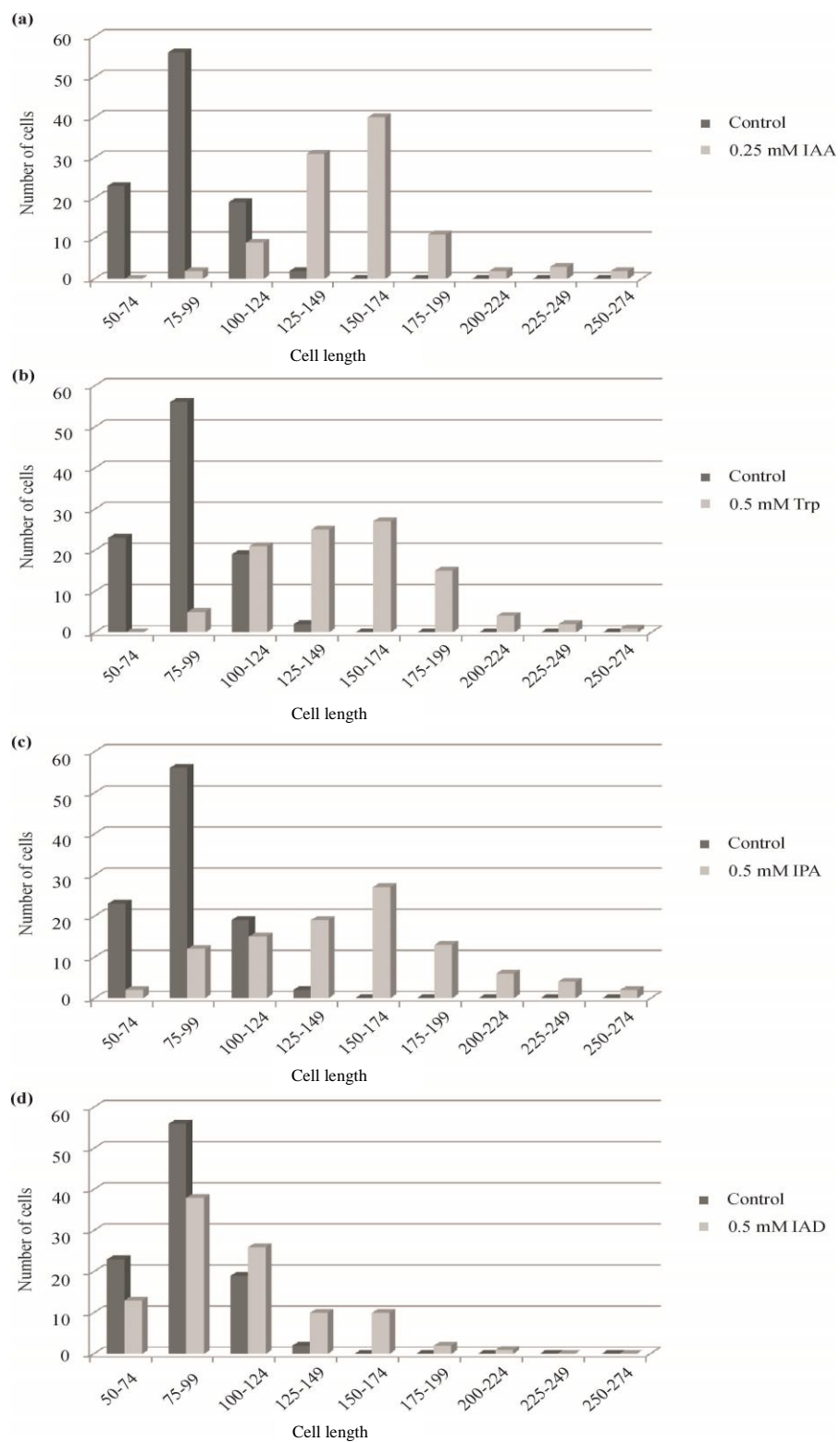


Fig. S3: Influence of IAA and precursors on cell length distribution. MMNb control was compared to 0.25 mM IAA (a), 0.5 mM Trp (b), 0.5 mM IPA (c) and 0.5 mM IAD (d) treatments.

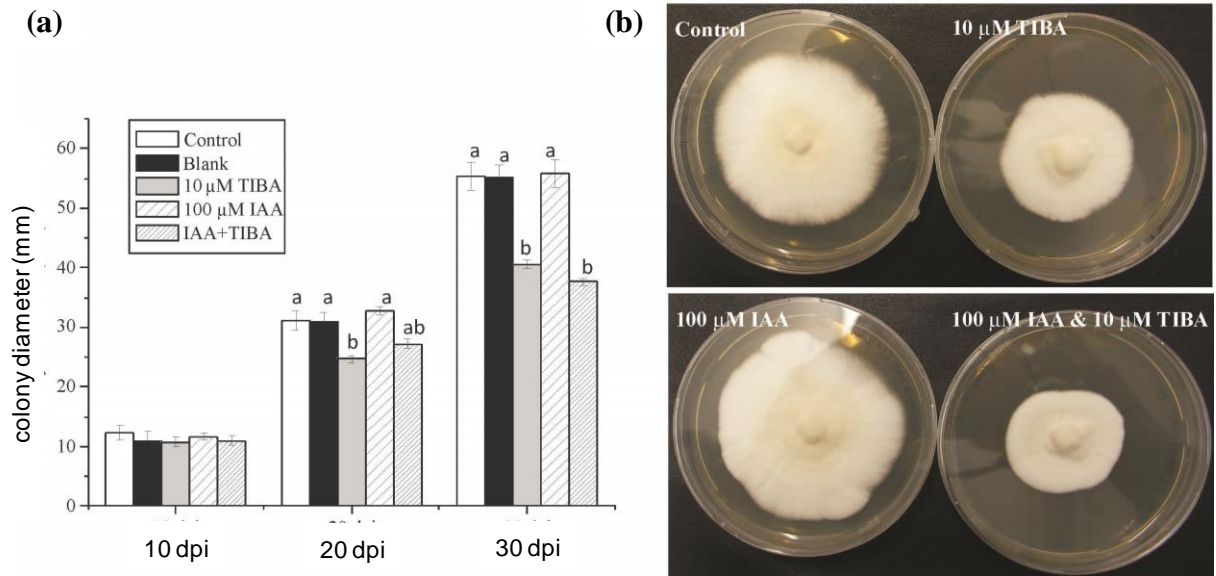


Fig. S4: Growth of *T. vaccinum* after 4-week application of IAA with or without addition of TIBA blocking IAA uptake. Fungal growth was measured as colony diameter, bars denote standard error, letters indicate significant differences (a); representative plate cultures (b).

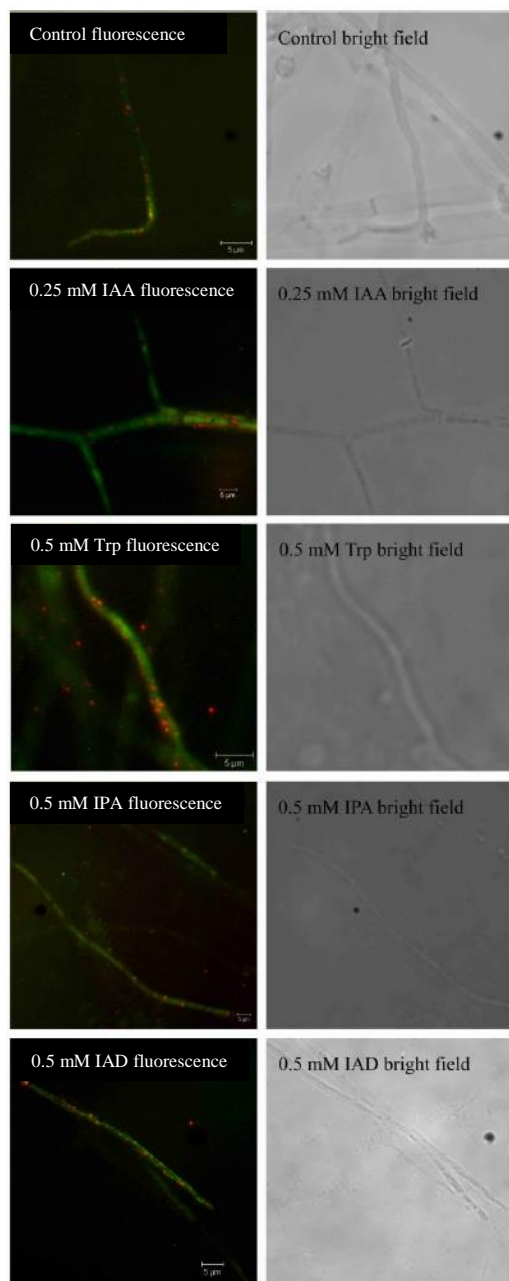


Fig. S5: Cytoskeleton of hyphae of *T. vaccinum* stained with immunofluorescence for actin (red) and tubulin (green) after treatment with 0.25 mM IAA and 0.5 mM of different IAA precursors in the tryptophan dependent pathway. Corresponding bright field picture is given on the right side.